

Serial Number: 09/9/0, 087**ENTERED**

O/R #2

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings-used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☒ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

Examiner: Am The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

## RAW SEQUENCE LISTING

DATE: 09/09/2001

PATENT APPLICATION: US/09/910,087

TIME: 18:50:52

Input Set : A:\Pto.amc

Output Set: N:\CRF3\09072001\I910087.raw

## SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:  
7 (i) APPLICANT: Koopman, Peter  
8 Goodfellow, Peter  
C--> 10 (ii) TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND  
11 USE IN THE REGENERATION OF BONE OR CARTILAGE  
13 (iii) NUMBER OF SEQUENCES: 21  
15 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: Scully, Scott, Murphy & Presser  
17 (B) STREET: 400 Garden City Plaza  
18 (C) CITY: Garden City  
19 (D) STATE: NY  
20 (E) COUNTRY: U.S.A.  
21 (F) ZIP: 11530  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Diskette  
25 (B) COMPUTER: IBM Compatible  
26 (C) OPERATING SYSTEM: DOS  
27 (D) SOFTWARE: FastSEQ Version 1.5  
29 (vi) CURRENT APPLICATION DATA:  
C--> 30 (A) APPLICATION NUMBER: US/09/910,087  
C--> 31 (B) FILING DATE: 20-Jul-2001  
32 (C) CLASSIFICATION:  
34 (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: AU PM9714  
36 (B) FILING DATE: 29-NOV-1994  
38 (A) APPLICATION NUMBER: AU PM9835  
39 (B) FILING DATE: 05-DEC-1994  
41 (A) APPLICATION NUMBER: PCT/AU95/00799  
42 (B) FILING DATE: 29-NOV-1995  
44 (viii) ATTORNEY/AGENT INFORMATION:  
45 (A) NAME: DiGiglio, Frank S.  
46 (B) REGISTRATION NUMBER: 31,346  
47 (C) REFERENCE/DOCKET NUMBER: 10981  
49 (ix) TELECOMMUNICATION INFORMATION:  
50 (A) TELEPHONE: 516-742-4343  
51 (B) TELEFAX: 516-742-4366  
52 (C) TELEX:  
53 (2) INFORMATION FOR SEQ ID NO: 1:  
55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 7 base pairs  
57 (B) TYPE: nucleic acid  
58 (C) STRANDEDNESS: single  
59 (D) TOPOLOGY: linear  
61 (ii) MOLECULE TYPE: cDNA  
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
65 AATTAAA

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68 (2) INFORMATION FOR SEQ ID NO: 2:
70     (i) SEQUENCE CHARACTERISTICS:
71         (A) LENGTH: 19 base pairs
72         (B) TYPE: nucleic acid
73         (C) STRANDEDNESS: single
74         (D) TOPOLOGY: linear
76     (ii) MOLECULE TYPE: cDNA
78     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
80 CCAAAGTCCT AAAGGTGGG                                     19
83 (2) INFORMATION FOR SEQ ID NO: 3:
85     (i) SEQUENCE CHARACTERISTICS:
86         (A) LENGTH: 19 base pairs
87         (B) TYPE: nucleic acid
88         (C) STRANDEDNESS: single
89         (D) TOPOLOGY: linear
91     (ii) MOLECULE TYPE: cDNA
93     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
95 TTTCAGGCAA ATAAGGCAG                                     19
98 (2) INFORMATION FOR SEQ ID NO: 4:
100    (i) SEQUENCE CHARACTERISTICS:
101        (A) LENGTH: 20 base pairs
102        (B) TYPE: nucleic acid
103        (C) STRANDEDNESS: single
104        (D) TOPOLOGY: linear
106    (ii) MOLECULE TYPE: cDNA
108    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
110 TGGCAATCTA ACAGATGAGA                                     20
113 (2) INFORMATION FOR SEQ ID NO: 5:
115    (i) SEQUENCE CHARACTERISTICS:
116        (A) LENGTH: 20 base pairs
117        (B) TYPE: nucleic acid
118        (C) STRANDEDNESS: single
119        (D) TOPOLOGY: linear
121    (ii) MOLECULE TYPE: cDNA
123    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
125 TCNCAAATGT CATATATCCA                                     20
128 (2) INFORMATION FOR SEQ ID NO: 6:
130    (i) SEQUENCE CHARACTERISTICS:
131        (A) LENGTH: 22 base pairs
132        (B) TYPE: nucleic acid
133        (C) STRANDEDNESS: single
134        (D) TOPOLOGY: linear
136    (ii) MOLECULE TYPE: cDNA
138    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
140 AGTCCAGATT GACTGGAACA CA                                   22
143 (2) INFORMATION FOR SEQ ID NO: 7:
145    (i) SEQUENCE CHARACTERISTICS:
146        (A) LENGTH: 24 base pairs
147        (B) TYPE: nucleic acid

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148         (C) STRANDEDNESS: single
149         (D) TOPOLOGY: linear
151     (ii) MOLECULE TYPE: cDNA
153     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
155 GCAATAAGAT ACTAATATGT AGAG                                     24
157 (2) INFORMATION FOR SEQ ID NO: 8:
159     (i) SEQUENCE CHARACTERISTICS:
160         (A) LENGTH: 20 base pairs
161         (B) TYPE: nucleic acid
162         (C) STRANDEDNESS: single
163         (D) TOPOLOGY: linear
165     (ii) MOLECULE TYPE: cDNA
167     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
169 GTCAGCAGAA ATCTAAAGG                                           20
172 (2) INFORMATION FOR SEQ ID NO: 9:
174     (i) SEQUENCE CHARACTERISTICS:
175         (A) LENGTH: 20 base pairs
176         (B) TYPE: nucleic acid
177         (C) STRANDEDNESS: single
178         (D) TOPOLOGY: linear
180     (ii) MOLECULE TYPE: cDNA
182     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
184 GACTAATGCC GATGGTTAAG                                           20
187 (2) INFORMATION FOR SEQ ID NO: 10:
189     (i) SEQUENCE CHARACTERISTICS:
190         (A) LENGTH: 20 base pairs
191         (B) TYPE: nucleic acid
192         (C) STRANDEDNESS: single
193         (D) TOPOLOGY: linear
195     (ii) MOLECULE TYPE: cDNA
197     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
199 CGCCTCGAGG TGGCTTATCG                                           20
202 (2) INFORMATION FOR SEQ ID NO: 11:
204     (i) SEQUENCE CHARACTERISTICS:
205         (A) LENGTH: 25 base pairs
206         (B) TYPE: nucleic acid
207         (C) STRANDEDNESS: single
208         (D) TOPOLOGY: linear
210     (ii) MOLECULE TYPE: cDNA
212     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
214 ATCATACACA TACGATTTAG GTGAC                                     25
217 (2) INFORMATION FOR SEQ ID NO: 12:
219     (i) SEQUENCE CHARACTERISTICS:
220         (A) LENGTH: 19 base pairs
221         (B) TYPE: nucleic acid
222         (C) STRANDEDNESS: single
223         (D) TOPOLOGY: linear
225     (ii) MOLECULE TYPE: cDNA
227     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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229 GAGGAAGTCG GTGAAGAAC 19
232 (2) INFORMATION FOR SEQ ID NO: 13:
234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 21 base pairs
236 (B) TYPE: nucleic acid
237 (C) STRANDEDNESS: single
238 (D) TOPOLOGY: linear
240 (ii) MOLECULE TYPE: cDNA
242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
244 TCGCTCATGC CGGAGGAGGA G 21
247 (2) INFORMATION FOR SEQ ID NO: 14:
249 (i) SEQUENCE CHARACTERISTICS:
250 (A) LENGTH: 21 base pairs
251 (B) TYPE: nucleic acid
252 (C) STRANDEDNESS: single
253 (D) TOPOLOGY: linear
255 (ii) MOLECULE TYPE: cDNA
257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
259 GCAATCCCGAG GGCCACCGA C 21
261 (2) INFORMATION FOR SEQ ID NO: 15:
263 (i) SEQUENCE CHARACTERISTICS:
264 (A) LENGTH: 22 base pairs
265 (B) TYPE: nucleic acid
266 (C) STRANDEDNESS: single
267 (D) TOPOLOGY: linear
269 (ii) MOLECULE TYPE: cDNA
271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
273 TTGGAGATGA CGTCGACTGC TC 22
276 (2) INFORMATION FOR SEQ ID NO: 16:
278 (i) SEQUENCE CHARACTERISTICS:
279 (A) LENGTH: 20 base pairs
280 (B) TYPE: nucleic acid
281 (C) STRANDEDNESS: single
282 (D) TOPOLOGY: linear
284 (ii) MOLECULE TYPE: cDNA
286 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
288 GCAGCGACGT CATCTCCAAC 20
291 (2) INFORMATION FOR SEQ ID NO: 17:
293 (i) SEQUENCE CHARACTERISTICS:
294 (A) LENGTH: 21 base pairs
295 (B) TYPE: nucleic acid
296 (C) STRANDEDNESS: single
297 (D) TOPOLOGY: linear
299 (ii) MOLECULE TYPE: cDNA
301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
303 GCTGCTTGGA CATCCACACG T 21
306 (2) INFORMATION FOR SEQ ID NO: 18:
308 (i) SEQUENCE CHARACTERISTICS:
309 (A) LENGTH: 2249 base pairs

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310      (B) TYPE: nucleic acid
311      (C) STRANDEDNESS: single
312      (D) TOPOLOGY: linear
314      (ii) MOLECULE TYPE: cDNA
316      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
318  AGTTTCAGTC  CAGGAAC TTT  TCTTTGCAAG  AGAGACGAGG  TGCAAGTGGC      50
320  CCCGGTTTCG  TTCTCTG TTT  TCCCTCCCTC  CTCTCCGCT  CCGACTCGCC      100
322  TTCCCCGGGT  TTAGAGCCGG  CAGCTGAGAC  CCGCCACCCA  GCGCCTCTGC      150
324  TAAGTGCCCG  CCGCCGCAGC  CCGGTGACGC  GCCAACCTCC  CCGGGAGCCG      200
326  TTCGCTCGGC  GTCCGCGTCC  GGGCAGCTGA  GGGGAAGAGGA  GCCCCAGCCG      250
328  CCGCGGCTTC  TCGCCTTTCC  CGGCCACCCG  CCCCCTGCCC  CGGGCTCGCG      300
330  TATGAATCTC  CTGGACCCCT  TCATGAAGAT  GACCGACGAG  CAGGAGAAGG      350
332  GCCTGTCTGG  CGCCCCAGC  CCCACCATGT  CGGAGGACTC  GGCTGGTTCG      400
334  CCCTGTCCCT  CGGGCTCCGG  CTCGGACACG  GAGAACACCC  GGCCCCAGGA      450
336  GAACACCTTC  CCAAGGGCG  AGCCGGATCT  GAAGAAGGAG  AGCGAGGAAG      500
338  ATAAGTTCCT  CGTGTGCATC  CGCGAGGCGG  TCAGCCAGGT  GCTGAAGGGC      550
340  TACGACTGGA  CGCTGGTGCC  CATGCCCCTG  CGCGTCAACG  GCTCCAGCAA      600
342  GAACAAGCCA  CACGTCAAGC  GACCCATGAA  CGCCTTCATG  GTGTGGGCGC      650
344  AGGCTGCGCG  CAGGAAGCTG  GCAGACCAGT  ACCCGCATCT  GCACAACGCG      700
346  GAGCTCAGCA  AGACTCTGGG  CAAGCTCTGG  AGGCTGCTGA  ACGAGAGCGA      750
348  GAAGAGACCC  TTCGTGGAGG  AGGCGGAGCG  GCTGCGCGTG  CAGCACAAGA      800
350  AAGACCACCC  CGATTACAAG  TACCAGCCCC  GGCGGAGGAA  GTCGGTGAAG      850
352  AACGGACAAG  CGGAGGCCGA  AGAGGCCACG  GAACAGACTC  ACATCTCTCC      900
354  TAATGCTATC  TTCAAGGCGC  TGCAAGCCGA  CTCCCCACAT  TCCTCCTCCG      950
356  GCATGAGTGA  GGTGCACTCC  CCGGGCGAGC  ACTCTGGGGA  ATCTCAGGGT     1000
358  CCGCCGACCC  CACCCACCAC  TCCCAAAACC  GACGTGCAAG  CTGGCAAAGT     1050
360  TGATCTGAAG  CGAGAGGGGC  GCCCTCTGGC  AGAGGGGGGC  AGACAGCCCC     1100
362  CCATCGACTT  CCGCGACGTG  GACATCGGTG  AACTGAGCAG  CGACGTCATC     1150
364  TCCAACATTG  AGACCTTCGA  CGTCAATGAG  TTTGACCAAT  ACTTGCCACC     1200
366  CAACGGCCAC  CCAGGGGTTC  CGGCCACCCA  CGGCCAGGTC  ACCTACACTG     1250
368  GCAGTTACGG  CATCAGCAGC  ACCGCACCCA  CCCCTGCGAC  CGCGGGCCAC     1300
370  GTGTGGATGT  CGAAGCAGCA  GGCGCCGCCC  CCTCCTCCGC  AGCAGCCTCC     1350
372  GCAGGCCCCG  CAAGCCCCAC  AGGCGCCTCC  GCAGCAGCAA  GCACCCCGC      1400
374  AGCAGCCGCA  GGCACCCCAG  CAGCAGCAGG  CACACACGCT  CACCACGCTG     1450
376  AGCAGCGAGC  CAGGCCAGTC  CCAGCGAACG  CACATCAAGA  CGGAGCAGCT     1500
378  GAGCCCCAGC  CACTACAGGG  AGCAGCAGCA  GCACTCCCCG  CAACAGATCT     1550
380  CCTACAGCCC  CTTCAACCTT  CCTCACTACA  GGCCCTCCTA  CCCGCCCATC     1600
382  ACCCGTTCGG  AATACGACTA  CGCTGACCAT  CAGAACTCCG  GCTCCTACTA     1650
384  CAGTCACGCA  GCCGGCCAGG  GCTCAGGGCT  CTACTCCACC  TTCACTTACA     1700
386  TGAACCCCGC  GCAGCGCCCC  ATGTACACCC  CCATCGGTGA  CACCTCCGGG     1750
388  GTCCCTTCCA  TCCCGCAGAC  CCACAGCCCG  CAGGACTGGG  AACAACCACT     1800
390  CTACACACAG  GTCACCAGAC  CCTGAGAAGA  GAAAAGCTAT  GGTGACAGAG     1850
392  CTGATCTTTT  TTTTTTTTTT  TTTTAAAGA  AGAAAAGAAA  GAAACGAAAA     1900
394  AGAAAAAGCT  GAAGGAAATC  AAGAACCAAT  TGAAATTCCCT  TTGGACACTT     1950
396  TTTTTTTTGT  CCTTTCGTTA  ATTTTAAAA  GACATGTAAA  GGAAGGTAAC     2000
398  GATTGCTGGG  CATTCCAGGA  GAGAGACTTT  AAGACTTTGT  CTGAGCTCAT     2050
400  GACAACATAT  TGCAAAATGGC  CGGGCCACTC  GTGGCCAGAC  GGACAGCACT     2100
402  CCTGGCCAGA  TGGACCCACC  AGTATCAGCG  AGGAGGGGCT  TGTCTCCTTC     2150
404  AGAGTTAACA  TGGAGGACGA  TTGGAGAATC  TCCCTGCCTG  TTTGGACTTT     2200

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## VERIFICATION SUMMARY

DATE: 09/09/2001

PATENT APPLICATION: US/09/910,087

TIME: 18:50:53

Input Set : A:\Pto.amc

Output Set: N:\CRF3\09072001\I910087.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:417 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19